Please amend the application as follows to comply with requirements for patent applications containing nucleotide sequence and/or amino acid sequence disclosures in adherence with rules 37 C.F.R. § 1.821-1.825:

IN THE SPECIFICATION:

Please replace the paragraph beginning at page 3, line 3, with the following rewritten paragraph:

a1

– In one aspect, the present invention provides a recombinant nucleic acid encoding a cell cycle protein, termed "TaHo", which nucleic acid hybridizes under high stringency conditions to a nucleic acid comprising the nucleic acid sequence set forth in Figure 1 or Figure 2 (SEQ ID NOS:1, 2), or complements thereof.–

Please replace the paragraph beginning at page 3, line 8, with the following rewritten paragraph:

a2

– In one aspect, the present invention provides a recombinant nucleic acid encoding the TaHo cell cycle protein, which nucleic acid comprises a nucleic acid sequence having at least 85% identity to the nucleic acid sequence set forth in Figure 1 or Figure 2 (SEQ ID NOS:1, 2), or complements thereof.–

Please replace the paragraph beginning at page 3, line 12, with the following rewritten paragraph:

a3

– In a preferred embodiment, the present invention provides a recombinant nucleic acid encoding the TaHo cell cycle protein, which nucleic acid comprises the nucleic acid sequence set forth in Figure 1 or 2 (SEQ ID NOS:1, 2), or complements thereof.–

Please replace the paragraph beginning at page 3, line 19, with the following rewritten paragraph:

a4

– In one aspect, the present invention provides a recombinant nucleic acid encoding a cell cycle protein comprising the amino acid sequence set forth in Figure 3 or Figure 4 (SEQ ID NOS:3, 4).–

Please replace the paragraph beginning at page 3, line 35, with the following rewritten paragraph:

a5

– In one aspect, the present invention provides a recombinant cell cycle TaHo protein comprising an amino acid sequence having at least 85% identity to the sequence set forth in Figure 3 or Figure 4 (SEQ ID NOS:3, 4).–

Please replace the paragraph beginning at page 3, line 38, with the following rewritten paragraph:

a6

– In a preferred embodiment, the present invention provides a recombinant TaHo cell cycle protein comprising the amino acid sequence set forth in Figure 3 or Figure 4 (SEQ ID NOS:3, 4).–

Please replace the paragraph beginning at page 6, line 15, with the following rewritten paragraph:

a7

– Figure 8 shows a schematic representation of TaHo protein, depicting the ankyrin repeat domain, the SAM domain, and the PARP domain. The figure demonstrates schematically the relative position of TaHo amino acid sequence encoded by TaHo nucleic acid sequence to which antisense oligonucleotide is directed. The figure shows the nucleic acid sequence in this region (SEQ ID NO:5), and compares it to tankyrase nucleic acid sequence in the corresponding region of the tankyrase gene (SEQ ID NO:6). Asterisks indicate identical nucleotides in both the TaHo and tankyrase sequence. Depicted in bold text, and referred to by the term "T11" is the sequence of the TaHo antisense oligonucleotide (SEQ ID NO:7).

Please replace the paragraph beginning at page 7, line 9, with the following rewritten paragraph:

– Figure 16 shows the sequence of TaHo-1 (SEQ ID NO:8) and TaHo-2 (SEQ ID NO:9). The figure further identifies the E and F residues that are substituted and the amino acid sequences that are deleted in TaHo protein variants set forth (SEQ ID NOS:10-12). Also indicated are the amino acid sequences comprising ankyrin repeats, the SAM domain, and the PARP domain.–

Please replace the paragraph beginning at page 8, line 5, with the following rewritten paragraph:

– In one embodiment, the cell cycle protein is termed "tankyrase homolog", sometimes referred to herein as "tankyrase h" or "TaHo". The amino acid sequence is shown in Figure 3 and Figure 4 (SEQ ID NOS:3, 4), and the nucleic acid sequence is shown in Figure 1 and Figure 2 (SEQ ID NOS:1, 2). The amino acid sequence of tankyrase H bears homology to tankyrase, but preferably, less than 80%. Tankyrase is an enzyme which binds to TRF1 and which has been indicated as having a role in maintaining telomere length. Smith, et al., Science, 282(5393):1484-7 (1998). More particularly, tankyrase has homology to ankyrins and binds to the telomeric protein TRF1, a negative regulator of telomere length maintenance. Ankyrins have been reported to have homology to tissue-differentiation and cell cycle control proteins. Lux, et al., Nature, 344(6261):36-42 (1990). Telomeres shorten progressively with every cell division, ultimately causing cessation of cell division thereby inducing a cell death pathway. This process, telomeres, and the role of telomerase are further described in, e.g., Bryan and Cech, Curr Opin Cell Biol., 11(3):318-24 (1999); Hiyama, et al, Virchows Arch, 434(6):438-7 (1999); Krejc, Genomics, 58(2):202-6 (1999); Holt and Shay, J Cell Physiol., 180(1):10-8 (1999); and Tan, J Theor Biol., 198(2):259-68 (1999).–

Please replace the paragraph beginning at page 8, line 30, with the following rewritten paragraph:

– In one embodiment, the TaHo cell cycle nucleic acids or cell cycle proteins are initially identified by substantial nucleic acid and/or amino acid sequence identity or similarity to the sequence(s) provided herein. In a preferred embodiment, cell cycle nucleic acids or cell cycle proteins have sequence identity or similarity to the sequences provided herein as described below and one or more of the cell cycle protein bioactivities as further described below. Such sequence identity or similarity can be based upon the overall nucleic acid or amino acid sequence. A cell cycle protein, tankyrase H, is shown in and described in Figure 3 and Figure 4 (SEQ ID NOS:3, 4). –

Please replace the paragraph beginning at page 12, line 16, with the following rewritten paragraph:

– In a preferred embodiment, dominant negative TaHo protein isoforms are provided. Included and preferred among such TaHo proteins are proteins having mutations in an NAD+ binding site. More preferred among these proteins are those with F→L, or E→A, or F→L and E→A mutations in an NAD+ binding site, as those depicted in Figures 5 and 16 (SEQ ID NOS:10-12). Also preferred are TaHo proteins with deletions in the PARP domain at the C-terminus, preferably from amino acids 961-976, or amino acids 430-476, as set forth in Figure 16. Also highly preferred is a TaHo protein with such a C-terminus deletion from amino acids 961-976 as set forth in Figure 16, and having an E→A mutation or an F→L mutation or F→L and E→A mutations.–

Please replace the paragraph beginning at page 14, line 25, with the following rewritten paragraph:

– In a preferred embodiment, the present invention provides antisense oligonucleotides which find use as antagonists of TaHo activity. In a preferred embodiment, such antisense oligonucleotides are directed to the region in a TaHo nucleic acid intervening between the region encoding the

SAM domain and the region encoding the PARP domain. Particularly preferred are antisense oligonucleotides having a nucleic acids sequence complementary to the nucleic acid sequence GTGGAACAGAGGGTGCTTCC (SEQ ID NO:7). This is a preferred sequence for specific antisense targeting of TaHo as this sequence differs significantly from the nucleic acid sequence of the related tankyrase nucleic acid. As will be appreciated by those in the art, other TaHo nucleic acid sequence fragments that differ significantly from the sequence of tankyrase may be of use in the specific antisense targeting of TaHo. Alternatively, TaHo nucleic acid sequence fragments having high identity to tankyrase nucleic acid sequence fragments may be used to target both tankyrase and TaHo by antisense oligonucleotides.–

Please replace the paragraph beginning at page 39, line 6, with the following rewritten paragraph:

– Particularly preferred among such dominant negative cell cycle proteins are dominant negative TaHo proteins having mutations in an NAD+ binding site. More preferred among these proteins are those with F→L, E→A, or F→L and E→A amino acid substitutions in an NAD+ binding site, as those depicted in Figure 5. Also preferred are TaHo proteins with deletions in the PARP domain, preferably from amino acids 461-476 or 430-476 as depicted in Figure 16 (SEQ ID NOS:10-12). Also preferred is a TaHo protein with such a C-terminus deletion from amino acids 461-476 as set forth in Figure 16 and having an F→L, E→A, or F→L and E→A amino acid substitution in an NAD+ binding site, as depicted in Figure 16.–

Please replace the paragraph beginning at page 44, line 36, with the following rewritten paragraph:

– A number of cyclin destruction boxes are known in the art, for example, cyclin A has a destruction box comprising the sequence RTVLGVIGD (SEQ ID NO:13); the destruction box of cyclin B1 comprises the sequence RTALGDIGN (SEQ ID NO:14). See Glotzer et al., Nature

349:132-138 (1991). Other destruction boxes are known as well:

YMTVSIIDRFMQDSCVPKKMLQLVGVT (rat cyclin B; SEQ ID NO:15);

KFRLLQETMYMTVSIIDRFMQNSCVPKK (mouse cyclin B; SEQ ID NO:16);

RAILIDWLIQVQMKFRLLQETMYMTVS (mouse cyclin B1; SEQ ID NO:17);

DRFLQAQLVCRKKLQVVGITALLLASK (mouse cyclin B2; SEQ ID NO:18); and

MSVLRGKLQLVGTAAMLL (mouse cyclin A2; SEQ ID NO:19).–

Please replace the paragraph beginning at page 61, line 8, with the following rewritten paragraph:

– Oligonucleotides complementary to the TaHo nucleic acid sequence fragment GTGGAACAGAGGGTGCTTCC (Figure 8; SEQ ID NO:7) were transfected into A549 cells and Hela cells. These dominant negative oligonucleotides inhibited cell proliferation in both cell types, as depicted in Figures 9). Further, an increase in the amount of such TaHo antisense oligonucleotide was inversely correlated with the amount of TaHo mRNA detected in these cells, and was further correlated with the degree of proliferation inhibition observed (Figure 9).–

On page 63, immediately preceding the heading "CLAIMS," please insert the enclosed text entitled "SEQUENCE LISTING".

IN THE CLAIMS:

Please replace Claim 27 with the following rewritten claim:

– 27. (Amended) A method for screening for a candidate bioactive agent capable of modulating PARP activity, comprising the steps of:

(i) providing a TaHo protein;

(ii) providing a candidate bioactive agent; and